

Cdk5rap1 Cas9-CKO Strategy

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Design Date: 2021-6-11

Project Overview

Project Name

Cdk5rap1

Project type

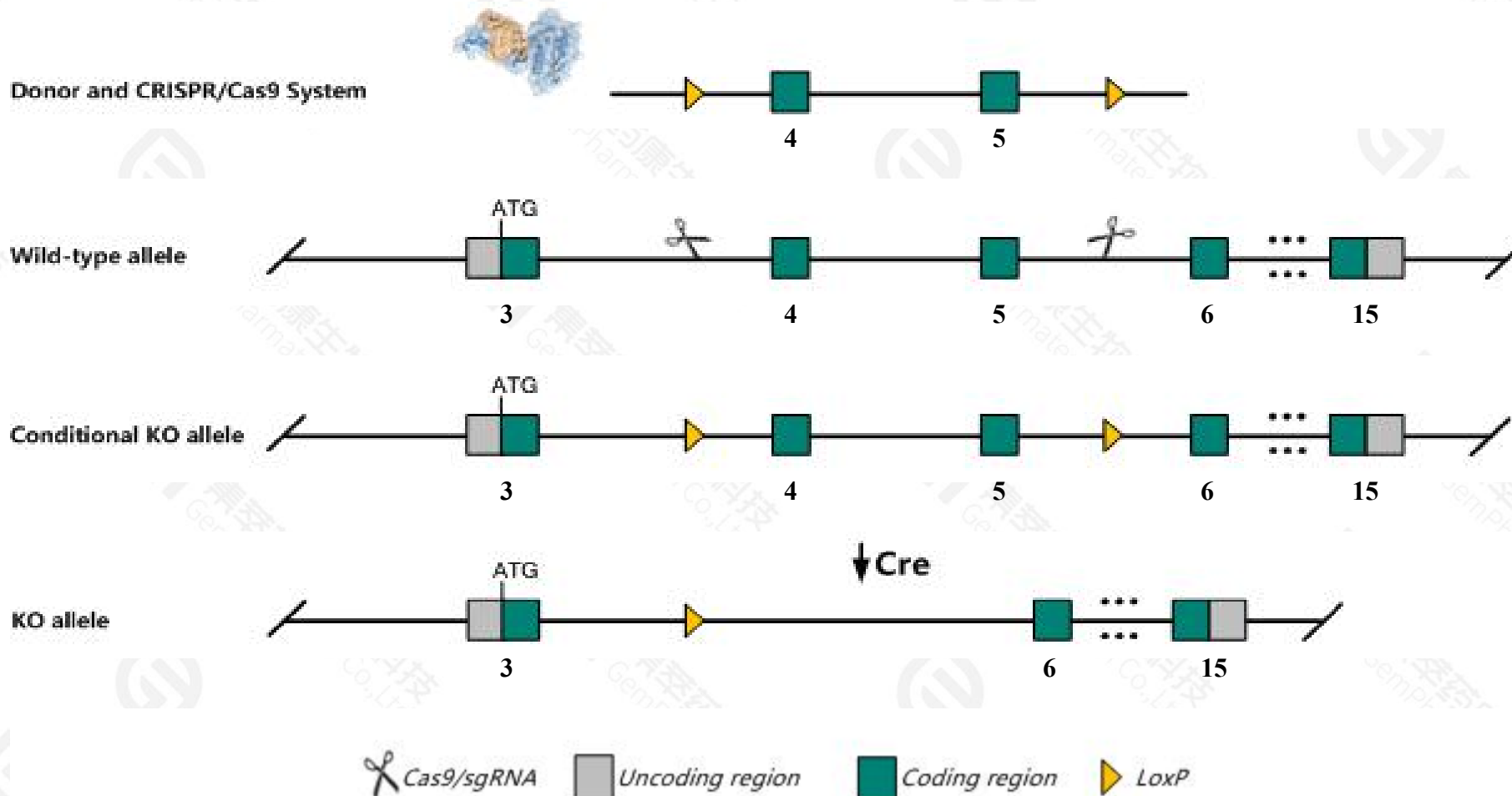
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cdk5rap1* gene. The schematic diagram is as follows:



Technical routes

- The *Cdk5rap1* gene has 7 transcripts. According to the structure of *Cdk5rap1* gene, exon4-exon5 of *Cdk5rap1*-203(ENSMUST00000109731.8) transcript is recommended as the knockout region. The region contains 139bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cdk5rap1* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor was constructed. Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, mice homozygous for a null allele show deficient mitochondrial tRNA modification, reduced mitochondrial protein synthesis, defects in oxidative phosphorylation, high susceptibility to stress-induced mitochondrial remodeling, and accelerated myopathy and cardiac dysfunction under stressed conditions.
- The *Cdk5rap1* gene is located on the Chr2. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Cdk5rap1 CDK5 regulatory subunit associated protein 1 [Mus musculus (house mouse)]

Gene ID: 66971, updated on 17-Nov-2020

Summary



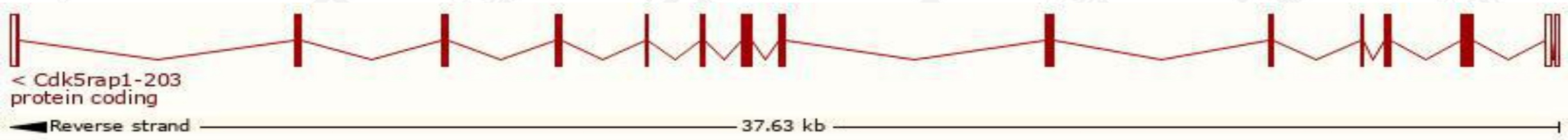
Official Symbol	Cdk5rap1 provided by MGI
Official Full Name	CDK5 regulatory subunit associated protein 1 provided by MGI
Primary source	MGI:MGI:1914221
See related	Ensembl:ENSMUSG00000027487
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310066P17Rik
Expression	Ubiquitous expression in placenta adult (RPKM 4.2), bladder adult (RPKM 3.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

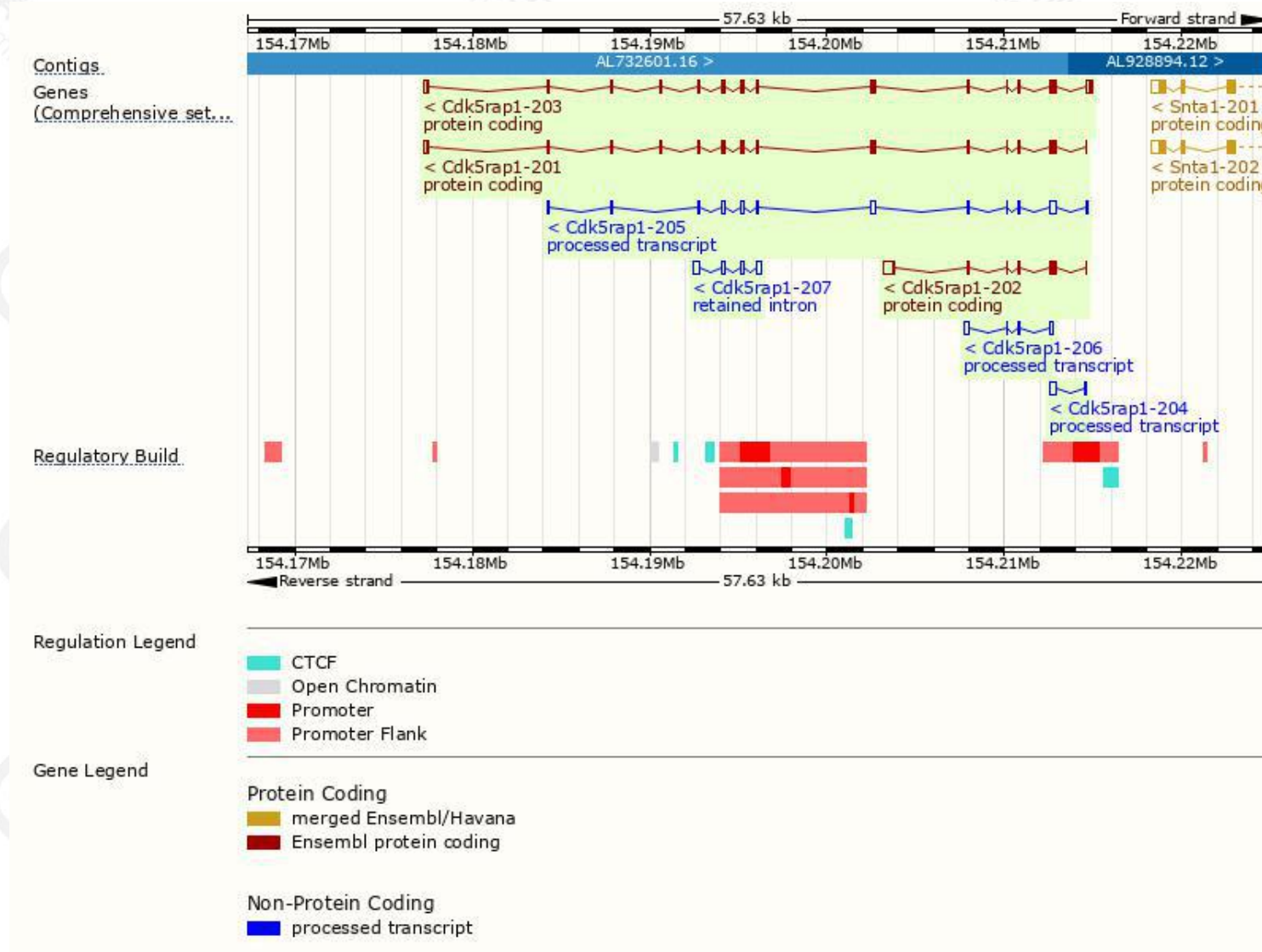
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cdk5rap1-203	ENSMUST00000109731.8	2160	588aa	Protein coding	CCDS16931		TSL:5 , GENCODE basic , APPRIS P1 ,
Cdk5rap1-201	ENSMUST00000028990.10	1970	588aa	Protein coding	CCDS16931		TSL:1 , GENCODE basic , APPRIS P1 ,
Cdk5rap1-202	ENSMUST00000109730.3	1227	190aa	Protein coding	-		TSL:1 , GENCODE basic ,
Cdk5rap1-205	ENSMUST00000148289.8	1649	No protein	Processed transcript	-		TSL:5 ,
Cdk5rap1-206	ENSMUST00000150308.2	515	No protein	Processed transcript	-		TSL:2 ,
Cdk5rap1-204	ENSMUST00000137918.2	392	No protein	Processed transcript	-		TSL:3 ,
Cdk5rap1-207	ENSMUST00000152180.2	936	No protein	Retained intron	-		TSL:3 ,

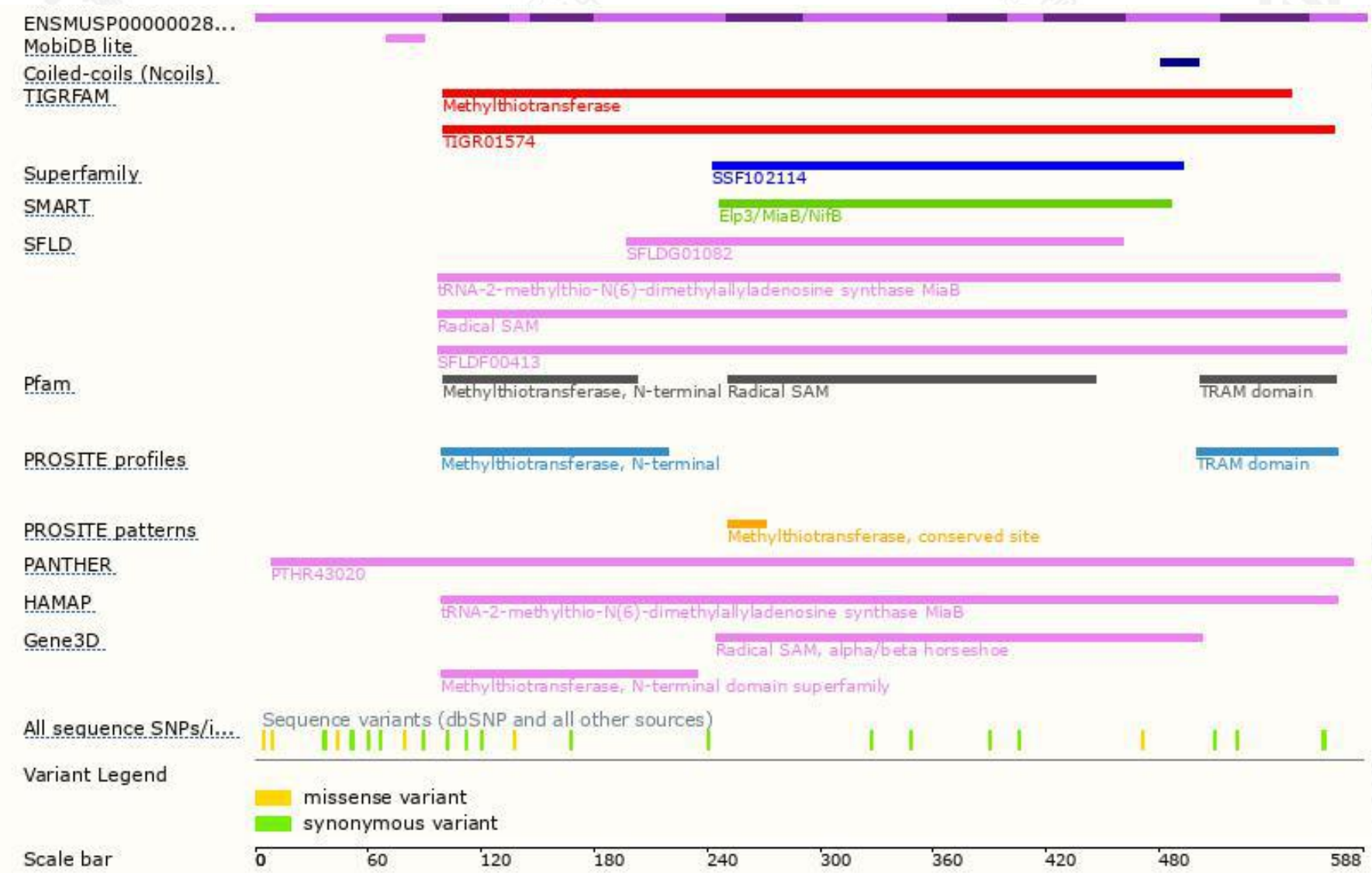
The strategy is based on the design of *Cdk5rap1-203* transcript,the transcription is shown below:



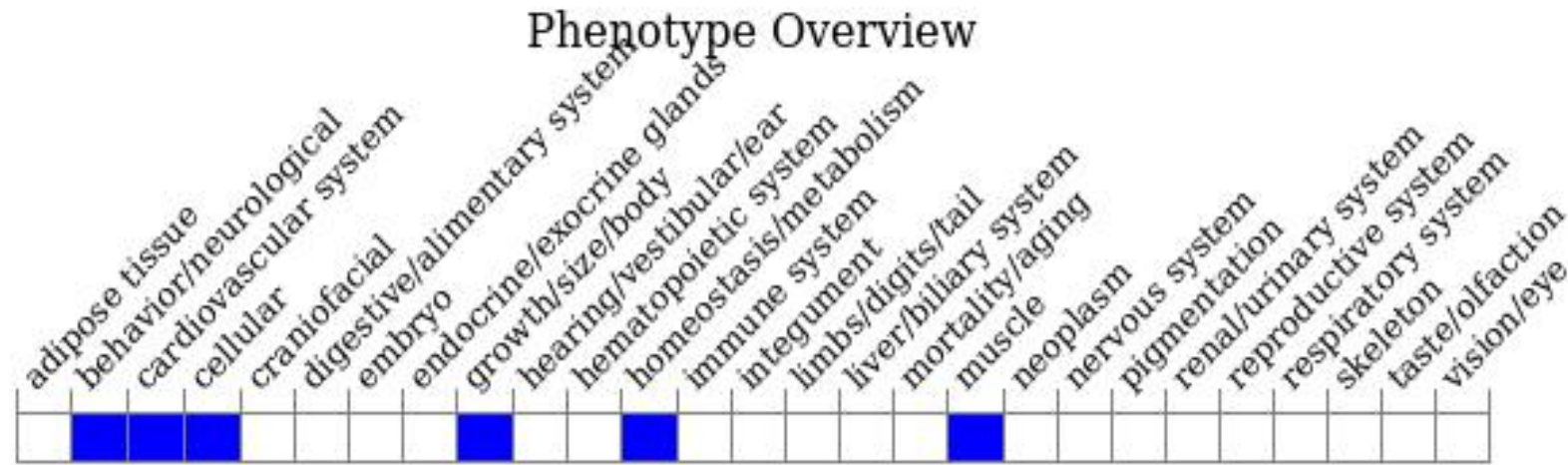
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, mice homozygous for a null allele show deficient mitochondrial tRNA modification, reduced mitochondrial protein synthesis, defects in oxidative phosphorylation, high susceptibility to stress-induced mitochondrial remodeling, and accelerated myopathy and cardiac dysfunction under stressed conditions.

If you have any questions, you are welcome to inquire.

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